

SEQUENCE LISTING

<110> Meyers, Rachel

<120> 50566, A NOVEL HUMAN GLYOXALASE II RELATED FACTOR AND
USES THEREOF

<130> MNI-185

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<150> 60/229,425

<151> 2000-08-31

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 1154

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (22) .. (870)

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Glu Gly Val Ser Leu Thr Ala Val Leu Thr Thr His His His Trp Asp
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cac gcg cgg gga aac cgg gag ctg gcg cgg ctt cgt ccc ggg ctg gcg 243
His Ala Arg Gly Asn Pro Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala
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gtg ctg ggc gcg gac gag cgc atc ttc tcg ctg acg cgc agg ctg gcg 291
Val Leu Gly Ala Asp Glu Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala
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cac ggc gag gag ctg cgg ttc ggg gcc atc cac gtg cgt tgc ctc ctg 339
His Gly Glu Glu Leu Arg Phe Gly Ala Ile His Val Arg Cys Leu Leu
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acg ccc ggc cac acc gcc ggc cac atg agc tac ttc ctg tgg gag gac 387
Thr Pro Gly His Thr Ala Gly His Met Ser Tyr Phe Leu Trp Glu Asp
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Ala Gly Cys Gly Ser Cys Leu Glu Gly Ser Ala Gln Gln Met Tyr Gln
140 145 150

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Ser Leu Ala Glu Leu Gly Thr Leu Pro Pro Glu Thr Lys Val Phe Cys
155 160 165 170

ggc cac gag cac acg ctt agc aac ctg gag ttt gcc cag aaa gtg gag 579
Gly His Glu His Thr Leu Ser Asn Leu Glu Phe Ala Gln Lys Val Glu
175 180 185

ccc tgc aac gac cac gtg aga gcc aag ctg tcc tgg gct aag aag agg 627
Pro Cys Asn Asp His Val Arg Ala Lys Leu Ser Trp Ala Lys Lys Arg
190 195 200

gat gag gat gac gtg ccc act gtg ccg tcg act ctg ggc gag gag cgc 675
Asp Glu Asp Asp Val Pro Thr Val Pro Ser Thr Leu Gly Glu Glu Arg
205 210 215

ctc tac aac ccc ttc ctg cgg gtg gca gag gag ccg gtg cgc aag ttc 723
Leu Tyr Asn Pro Phe Leu Arg Val Ala Glu Glu Pro Val Arg Lys Phe
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acg ggc aag gcg gtc ccc gcc gac gtc ctg gag gcg cta tgc aag gag 771
Thr Gly Lys Ala Val Pro Ala Asp Val Leu Glu Ala Leu Cys Lys Glu
235 240 245 250

cgg gcg cgc ttc gaa cag gcg ggc gag ccg cgg cag cca cag gcg cgg 819
Arg Ala Arg Phe Glu Gln Ala Gly Glu Pro Arg Gln Pro Gln Ala Arg
255 260 265

gcc ctc ctt gcg ctg cag tgg ggg ctc ctg agt gca gcc cca cac gac 867
Ala Leu Leu Ala Leu Gln Trp Gly Leu Leu Ser Ala Ala Pro His Asp
270 275 280

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ggccagctgg acccacatga gggccacctc tggaaccttc ttcgaggccc tggccagcca 980

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cagtggggcc tgtgtgggag ccgagacctg ggtgtctggg aagtggggca cacggggcct 1100

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Pro Lys Arg Leu Leu Glu Ile Val Gly Arg Glu Gly Val Ser Leu Thr
35 40 45

Ala Val Leu Thr Thr His His His Trp Asp His Ala Arg Gly Asn Pro
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Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala Val Leu Gly Ala Asp Glu
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Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala His Gly Glu Glu Leu Arg
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Phe Gly Ala Ile His Val Arg Cys Leu Leu Thr Pro Gly His Thr Ala
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Gly His Met Ser Tyr Phe Leu Trp Glu Asp Asp Cys Pro Asp Pro Pro
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165 170 175

Ser Asn Leu Glu Phe Ala Gln Lys Val Glu Pro Cys Asn Asp His Val
180 185 190

Arg Ala Lys Leu Ser Trp Ala Lys Lys Arg Asp Glu Asp Asp Val Pro
195 200 205

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Arg Val Ala Glu Glu Pro Val Arg Lys Phe Thr Gly Lys Ala Val Pro
225 230 235 240

Ala Asp Val Leu Glu Ala Leu Cys Lys Glu Arg Ala Arg Phe Glu Gln
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Val Ile Glu Glu Leu Thr Arg Glu Ala Val Ala Val Asp Val Ala Val
      20              25              30

ccc aag agg ctg ctg gag atc gtg ggc cgg gag ggg gtg tct ctg acc 144
Pro Lys Arg Leu Leu Glu Ile Val Gly Arg Glu Gly Val Ser Leu Thr
      35              40              45

gct gtg ctg acc acc cac cat cac tgg gac cac gcg cgg gga aac ccg 192
Ala Val Leu Thr Thr His His Trp Asp His Ala Arg Gly Asn Pro
      50              55              60

gag ctg gcg cgg ctt cgt ccc ggg ctg gcg gtg ctg ggc gcg gac gag 240
Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala Val Leu Gly Ala Asp Glu
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cgc atc ttc tcg ctg acg cgc agg ctg gcg cac ggc gag gag ctg cgg 288
Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala His Gly Glu Glu Leu Arg
      85              90              95

ttc ggg gcc atc cac gtg cgt tgc ctc ctg acg ccc ggc cac acc gcc 336
Phe Gly Ala Ile His Val Arg Cys Leu Leu Thr Pro Gly His Thr Ala
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Gly His Met Ser Tyr Phe Leu Trp Glu Asp Asp Cys Pro Asp Pro Pro
      115              120              125

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Ala Leu Phe Ser Gly Asp Ala Leu Ser Val Ala Gly Cys Gly Ser Cys
      130              135              140

ctg gag ggc agc gcc cag cag atg tac cag agc ctg gcc gag ctg ggt 480
Leu Glu Gly Ser Ala Gln Gln Met Tyr Gln Ser Leu Ala Glu Leu Gly
      145              150              155              160

acc ctg ccc ccc gag acg aag gtg ttc tgc ggc cac gag cac acg ctt 528
Thr Leu Pro Pro Glu Thr Lys Val Phe Cys Gly His Glu His Thr Leu
      165              170              175

agc aac ctg gag ttt gcc cag aaa gtg gag ccc tgc aac gac cac gtg 576
Ser Asn Leu Glu Phe Ala Gln Lys Val Glu Pro Cys Asn Asp His Val
      180              185              190

aga gcc aag ctg tcc tgg gct aag aag agg gat gag gat gac gtg ccc 624
Arg Ala Lys Leu Ser Trp Ala Lys Lys Arg Asp Glu Asp Asp Val Pro
      195              200              205

act gtg ccg tcg act ctg ggc gag gag cgc ctc tac aac ccc ttc ctg 672
Thr Val Pro Ser Thr Leu Gly Glu Glu Arg Leu Tyr Asn Pro Phe Leu
      210              215              220

cgg gtg gca gag gag ccg gtg cgc aag ttc acg ggc aag gcg gtc ccc 720
Arg Val Ala Glu Glu Pro Val Arg Lys Phe Thr Gly Lys Ala Val Pro
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gcg ggc gag ccg cgg cag cca cag gcg cgg gcc ctc ctt gcg ctg cag	816
Ala Gly Glu Pro Arg Gln Pro Gln Ala Arg Ala Leu Leu Ala Leu Gln	
260 265 270	
tgg ggg ctc ctg agt gca gcc cca cac gac	846
Trp Gly Leu Leu Ser Ala Ala Pro His Asp	
275 280	